

# SEQUENCE ALIGNMENT OF SEQ ID NO: 2 AND 4 AGAINST

## HUMAN $\gamma$ -HEREGULIN

RESULT 9

AAW44817

ID AAW44817 standard; Protein; 768 AA.

XX

AC AAW44817;

XX

DT 17-AUG-1998 (first entry)

XX

DE Human gamma-hereregulin.

XX

KW Gamma-hereregulin; gamma-HRG; human; autocrine growth factor;

KW breast cancer; MDA-MB-175 cell; diagnosis; gene therapy;

KW ErbB receptor; cell proliferation; cell differentiation;

KW cell survival; neurological disorder; muscular disorder.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Domain 1..560

FT /note= "N-terminal domain (Claim 5)"

FT Region 342..363

FT /note= "hydrophobic region, may function as  
internal signal sequence"

FT Domain 704..748

FT /note= "EGF-like domain"

FT Modified-site 77

FT /note= "N-glycosylated"

FT Modified-site 151

FT /note= "N-glycosylated"

FT Modified-site 467

FT /note= "N-glycosylated"

FT Modified-site 647

FT /note= "N-glycosylated"

FT Modified-site 653

FT /note= "N-glycosylated"

FT Modified-site 691

FT /note= "N-glycosylated"

XX

PN WO9802541-A1.

XX

PD 22-JAN-1998.

XX

PF 08-JUL-1997; 97WO-US11841.

XX

PR 12-JUL-1996; 96US-0021640.

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PA (GETH ) GENENTECH INC.

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PI Schaefer GM, Sliwkowski M;

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DR WPI; 1998-110589/10.

DR N-PSDB; AAV19251.

XX

PT DNA encoding gamma-hereregulin - used to activate ErbB receptor and to

PT enhance proliferation, differentiation or survival of a cell

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PS Claim 3; Fig 1A-C; 81pp; English.

XX

CC This polypeptide comprises human gamma-hereregulin (gamma-HRG), a

CC novel member of the hereregulin superfamily, that has a unique

CC N-terminal domain not present in previously identified hereregulins.

CC Gamma-HRG is secreted by human breast cancer MDA-MB-175 cells. It

CC leads to the formation of a constitutive active receptor complex

CC and stimulates the growth of these cells in an autocrine manner.

CC A claimed method for activating an ErbB receptor comprises contact

CC a cell which expresses the receptor with gamma-HRG. A claimed

CC method for enhancing the proliferation, differentiation or survival

CC of a cell, especially a glial cell or muscle, comprises contacting

CC the cell with gamma-HRG. Antibodies raised against the unique

CC N-terminal domain of gamma-HRG can be used to detect and purify

CC the protein. Antagonists of gamma-HRG can be used to block

CC gamma-HRG activity and expression. The gamma-HRG may be obtained  
CC from claimed host cells that comprise a vector containing an  
CC isolated gamma HRG nucleic acid (see AAV19251).  
XX  
SQ Sequence 768 AA;

Query Match 20.3%; Score 3003; DB 19; Length 768;  
Best Local Similarity 76.7%; Pred. No. 9.7e-161;  
Matches 600; Conservative 22; Mismatches 82; Indels 78; Gaps 10;

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Qy      1 MDVKERKPYRSLTRRRDAERRYSSSSADSEEGKAPQKSYSSSETLKAYDQDARLAYGSRV 60
      |||
Db      1 MDVKERKPYRSLTRRRDAERRYSSSSADSEEGKAPQKSYSSSETLKAYDQDARLAYGSRV 60

Qy     61 KDIVPQEAEEFCRTGANFTLRELGLEEVTPPHGTLYRTDIGLPHCGYSMGAGSDADMEAD 120
      |||
Db     61 KDIVPQEAEEFCRTGANFTLRELGLEEVTPPHGTLYRTDIGLPHCGYSMGAGSDADMEAD 120

Qy    121 TVLSPEHPVRLWGRSTRSGRSSCLSSRANSNLTLTDEHENTETDHPGGLQNHARLRTPP 180
      |||
Db    121 TVLSPEHPVRLWGRSTRSGRSSCLSSRANSNLTLTDEHENTETDHPGGLQNHARLRTPP 180

Qy    181 PPLSHAHTPNQHAASINSLNRGNFTPRSNPSPAPTDHSLSGEPPAGGAQEPAAHQENWL 240
      |||
Db    181 PPLSHAHTPNQHAASINSLNRGNFTPRSNPSPAPTDHSLSGEPPAGGAQEPAAHQENWL 240

Qy    241 LNSNIPLSTRNLGKQPFGLTLDNLIEMDILGASRHDGAYS DGHFLFKPGGTSPLFCTTS 300
      |||
Db    241 LNSNIPLSTRNLGKQPFGLTLDNLIEMDILGASRHDGAYS DGHFLFKPGGTSPLFCTTS 300

Qy    301 PGYPLTSSTVYSPPPRPLPRSTFARPAFNLKKPSKYCNWKAALSAIVISATLVILLAYF 360
      |||
Db    301 PGYPLTSSTVYSPPPRPLPRSTFARPAFNLKKPSKYCNWKAALSAIVISATLVILLAYF 360

Qy    361 VAMHLFGLNWLQPMEGQMYEITEDTASSWPVPTDVS LYPSSGGTGLET PDRKGKGTTGK 420
      |||
Db    361 VAMHLFGLNWLQPMEGQMYEITEDTASSWPVPTDVS LYPSSGGTGLET PDRKGKGTTGK 420

Qy    421 PSSFFPEDSFIDSGEIDVGRRASQKIPPGTFWRSQVFI DHPVHLKFNVS LGAALVGIYG 480
      |||
Db    421 PSSFFPEDSFIDSGEIDVGRRASQKIPPGTFWRSQVFI DHPVHLKFNVS LGAALVGIYG 480

Qy    481 RKGLPPSHTQDFVELLDGRRLLTQEARSLEGT PRQSRGTVPSSHETGFIQYLD SGIWH 540
      |||
Db    481 RKGLPPSHTQDFVELLDGRRLLTQEARSLEGT PRQSRGTVPSSHETGFIQYLD SGIWH 540

Qy    541 LAFYNDGKESEVVSFLTTAI---ESVDNCP SNCYGN GD-----CISGTCHCFLGFL---- 588
      |||
Db    541 LAFYNDGKESEVVSFLTTAIALPPRLKEMKQESAAGSKLVLRCE TSSEYSSLRFKWFKN 600

Qy    589 GPD CGRASC P-----VLCSGNGQYMKGRCLCHSGWKGAEC DVPTNQC 630
      | : | : |
Db    601 GNELNRKNKPQNIKI QKKPGKSEL RINKASLADSGEYM-----CKVISKLG 646

Qy    631 IDVACSNHGTCTGTCTICNPGYKGESCEEVD CMDPTCSGRGVCVRGECHCSVGWGGTNCE 690
      || : ||
Db    647 NDSASAN----ITIV-----ESNEIITGMPASTEGAYVSSESPIRISVSTEGANTS 693

Qy    691 TPRAT-----CLDQ-----CSGHGTFL-----PDTGLCSCDPSWTHDCSIEIC 729
      : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : |
Db    694 SSTSTSTGTSHLVKCAEKEKTF CVNGGECFMVKDLSNPSRYLCKCPNEFTGDRCQNYVM 753

Qy    730 AA 731
      | :
Db    754 AS 755
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